

DT05 Rec'd PCT/PTO 18 FEB 2005

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## SEQUENCE LISTING

5 <110> SunGene GmbH & Co. KGaA

10 <120> Process for preparing ketocarotenoids in genetically modified organisms

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20 <170> PatentIn version 3.1

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 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
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	cta gct gta geg ctt tac gct gtg ttt cca tat caa cag atg tta aag	336
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 Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro  
 1 5 10 15

10 gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96  
 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val  
 20 25 30

15 att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144  
 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp  
 35 40 45

atc tca aag att cat aag tgg atg tta ttg cct gtt ata cta tgg caa 192  
 Ile Ser Lys Ile His Lys Trp Met Leu Leu Pro Val Ile Leu Trp Gln  
 50 55 60

20 aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240  
 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His  
 65 70 75 80

25 ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca 288  
 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr  
 85 90 95

30 ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa 336  
 Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys  
 100 105 110

35 aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat 384  
 Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp  
 115 120 125

ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt 432  
 Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe  
 130 135 140

40 atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att 480  
 Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile  
 145 150 155 160

45 tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act 528  
 Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr  
 165 170 175

50 tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat 576  
 Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
 180 185 190

ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag 624

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
 195 200 205

5 cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc 672  
 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
 210 215 220

10 acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat 720  
 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
 225 230 235 240

15 att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag 762  
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 245 250

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30 Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro  
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35 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val  
 20 25 30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp  
 35 40 45

40 Ile Ser Lys Ile His Lys Trp Met Leu Leu Pro Val Ile Leu Trp Gln  
 50 55 60

45 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His  
 65 70 75 80

50 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr  
 85 90 95

## 20

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys  
 100 105 110

5 Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp  
 115 120 125

10 Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe  
 130 135 140

15 Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile  
 145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr  
 165 170 175

20 Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
 180 185 190

25 Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
 195 200 205

30 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
 210 215 220

35 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
 225 230 235 240

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys  
 245 250

40 <210> 13  
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45 <212> DNA  
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50 <220>

&lt;221&gt; CDS

&lt;222&gt; (1)..(762)

5 &lt;223&gt;

&lt;400&gt; 13

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	Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro	
	1 5 10 15	
15	gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc	96
	Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val	
	20 25 30	
20	att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac	144
	Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp	
	35 40 45	
25	atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa	192
	Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln	
	50 55 60	
30	aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat	240
	Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His	
	65 70 75 80	
35	ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca	288
	Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr	
	85 90 95	
40	ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa	336
	Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys	
	100 105 110	
45	aaa cat tgg tta cac cac cac aat cca gca agc gat tta gac ccg gat	384
	Lys His Trp Leu His His His Asn Pro Ala Ser Asp Leu Asp Pro Asp	
	115 120 125	
50	ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt	432
	Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe	
	130 135 140	
55	atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att	480
	Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile	
	145 150 155 160	
60	tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act	528
	Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr	
	165 170 175	

5    'tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat    576  
      Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
              180                                185                                190

10    ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag    624  
      Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
              195                                200                                205

15    cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc    672  
      Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
              210                                215                                220

20    acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat    720  
      Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
              225                                230                                235                                240

25    att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag    762  
      Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys  
              245                                250

30    <210> 14  
      <211> 253  
      <212> PRT  
      <213> Artificial sequence

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40    Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val  
              20                                25                                30

45    Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp  
              35                                40                                45

50    Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln  
              50                                55                                60

55    Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His  
      65                                70                                75                                80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr  
 85 90 95  
 5  
 Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys  
 100 105 110  
 10  
 Lys His Trp Leu His His His Asn Pro Ala Ser Asp Leu Asp Pro Asp  
 115 120 125  
 15  
 Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe  
 130 135 140  
 20  
 Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile  
 145 150 155 160  
 25  
 Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr  
 165 170 175  
 30  
 Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
 180 185 190  
 35  
 Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
 195 200 205  
 40  
 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
 210 215 220  
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 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
 225 230 235 240  
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 Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys  
 245 250  
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&lt;213&gt; Haematococcus pluvialis

5 &lt;220&gt;

&lt;221&gt; CDS

10

&lt;222&gt; (3)..(971)

&lt;223&gt;

15 &lt;400&gt; 15

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 Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile  
 1 5 10 15

20 ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95  
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu  
 20 25 30

25 tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc 143  
 Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala  
 35 40 45

30 cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg 191  
 Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser  
 50 55 60

35 tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga 239  
 Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly  
 65 70 75

acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca 287  
 Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala  
 80 85 90 95

40 ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa 335  
 Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys  
 100 105 110

45 cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc 383  
 Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly  
 115 120 125

50 gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac 431  
 Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His  
 130 135 140

atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc 479



25

	Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu	
	145 150 155	
5	ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr	527
	160 165 170 175	
10	gca cac aaa gcc atc tgg cat gag tgc cct ctg ggc tgg ctg ctg cac Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His	575
	180 185 190	
15	aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu	623
	195 200 205	
	ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly	671
	210 215 220	
20	ttc tgg ctg ccc aac qtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu	719
	225 230 235	
25	ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu	767
	240 245 250 255	
30	gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met	815
	260 265 270	
35	aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly	863
	275 280 285	
	ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile	911
	290 295 300	
40	cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp	959
	305 310 315	
45	tcc aag cgg tag ggtgcggaac caggcacgct ggtttcacac ctcatgcctg Ser Lys Arg	1011
	320	
	tgataaggtg tggctagagc gatgcgtgtg agacgggtat gtcacggtcg actggtctga	1071
50	tggccaatgg catcggccat gtctggtcat cacgggctgg ttgcctgggt gaaggtgatg	1131
	cacatcatca tgtgcggttg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc	1191

5 'caggctggcg ttgaatcagt gagggtttgt gattggcggt tgtgaagcaa tgactccgcc 1251  
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 10 agacgtagac cttgactgga ggcttgatcg agagagtggg ccgtattctt tgagagggga 1491  
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 Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu Ser  
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 35 Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala Arg  
 35 40 45  
 40 Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu  
 50 55 60  
 45 Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr  
 65 70 75 80  
 50 Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu  
 85 90 95

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg  
 100 105 110

5 Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val  
 115 120 125

10 Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met  
 130 135 140

15 Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu  
 145 150 155 160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala  
 165 170 175

20 His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys  
 180 185 190

25 Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe  
 195 200 205

30 Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe  
 210 215 220

35 Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly  
 225 230 235 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val  
 245 250 255

40 His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys  
 260 265 270

45 Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly  
 275 280 285

50 Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro  
 290 295 300

Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser  
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5 Lys Arg

10 <210> 17

<211> 1650

<212> DNA

15 <213> Lycopersicon esculentum

20 <220>

<221> CDS

<222> (112)..(1614)

25 <223>

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 aggaccccat ttgaagtttt cttgaaacaa atattaccct gttggaaaaa g atg gat 117  
 Met Asp  
 1

35  
 act ttg ttg aaa acc cca aat aac ctt gaa ttt ctg aac cca cat cat 165  
 Thr Leu Leu Lys Thr Pro Asn Asn Leu Glu Phe Leu Asn Pro His His  
 5 10 15

40 ggt ttt gct gtt aaa gct agt acc ttt aga tct gag aag cat cat aat 213  
 Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His His Asn  
 20 25 30

45 ttt ggt tct agg aag ttt tgt gaa act ttg ggt aga agt gtt tgt gtt 261  
 Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val Cys Val  
 35 40 45 50

50 aag ggt agt agt agt gct ctt tta gag ctt gta cct gag acc aaa aag 309  
 Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr Lys Lys  
 55 60 65

gag aat ctt gat ttt gag ctt cct atg tat gac cct tca aaa ggg gtt 357

	Glu	Asn	Leu	Asp	Phe	Glu	Leu	Pro	Met	Tyr	Asp	Pro	Ser	Lys	Gly	Val	
			70						75					80			
5	ggt	gtg	gat	ctt	gct	gtg	ggt	ggt	ggc	cct	gca	gga	ctt	gct	ggt		405
	Val	Val	Asp	Leu	Ala	Val	Val	Gly	Gly	Gly	Pro	Ala	Gly	Leu	Ala	Val	
			85					90					95				
10	gca	cag	caa	ggt	tct	gaa	gca	gga	ctc	tct	ggt	tgt	tca	att	gat	ccg	453
	Ala	Gln	Gln	Val	Ser	Glu	Ala	Gly	Leu	Ser	Val	Cys	Ser	Ile	Asp	Pro	
			100					105					110				
15	aat	cct	aaa	ttg	ata	tgg	cct	aat	aac	tat	ggt	ggt	tgg	gtg	gat	gaa	501
	Asn	Pro	Lys	Leu	Ile	Trp	Pro	Asn	Asn	Tyr	Gly	Val	Trp	Val	Asp	Glu	
	115					120					125					130	
20	ttt	gag	gct	atg	gac	ttg	tta	gat	tgt	cta	gat	gct	acc	tgg	tct	ggt	549
	Phe	Glu	Ala	Met	Asp	Leu	Leu	Asp	Cys	Leu	Asp	Ala	Thr	Trp	Ser	Gly	
						135					140				145		
25	gca	gca	gtg	tac	att	gat	gat	aat	acg	gct	aaa	gat	ctt	cat	aga	cct	597
	Ala	Ala	Val	Tyr	Ile	Asp	Asp	Asn	Thr	Ala	Lys	Asp	Leu	His	Arg	Pro	
						150				155					160		
30	tat	gga	agg	ggt	aac	cgg	aaa	cag	ctg	aaa	tcg	aaa	atg	atg	cag	aaa	645
	Tyr	Gly	Arg	Val	Asn	Arg	Lys	Gln	Leu	Lys	Ser	Lys	Met	Met	Gln	Lys	
			165					170					175				
35	tgt	ata	atg	aat	ggt	ggt	aaa	ttc	cac	caa	gcc	aaa	ggt	ata	aag	gtg	693
	Cys	Ile	Met	Asn	Gly	Val	Lys	Phe	His	Gln	Ala	Lys	Val	Ile	Lys	Val	
			180					185					190				
40	att	cat	gag	gaa	tcg	aaa	tcc	atg	ttg	ata	tgc	aat	gat	ggt	aft	act	741
	Ile	His	Glu	Glu	Ser	Lys	Ser	Met	Leu	Ile	Cys	Asn	Asp	Gly	Ile	Thr	
	195					200					205					210	
45	att	cag	gca	acg	gtg	gtg	ctc	gat	gca	act	ggc	ttc	tct	aga	tct	ctt	789
	Ile	Gln	Ala	Thr	Val	Val	Leu	Asp	Ala	Thr	Gly	Phe	Ser	Arg	Ser	Leu	
						215					220				225		
50	ggt	cag	tat	gat	aag	cct	tat	aac	ccc	ggg	tat	caa	ggt	gct	tat	ggc	837
	Val	Gln	Tyr	Asp	Lys	Pro	Tyr	Asn	Pro	Gly	Tyr	Gln	Val	Ala	Tyr	Gly	
						230				235				240			
55	att	ttg	gct	gaa	gtg	gaa	gag	cac	ccc	ttt	gat	gta	aac	aag	atg	ggt	885
	Ile	Leu	Ala	Glu	Val	Glu	Glu	His	Pro	Phe	Asp	Val	Asn	Lys	Met	Val	
			245					250					255				
60	ttc	atg	gat	tgg	cga	gat	tct	cat	ttg	aag	aac	aat	act	gat	ctc	aag	933
	Phe	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Lys	Asn	Asn	Thr	Asp	Leu	Lys	
			260					265					270				
65	gag	aga	aat	agt	aga	ata	cca	act	ttt	ctt	tat	gca	atg	cca	ttt	tca	981

## 30

	Glu	Arg	Asn	Ser	Arg	Ile	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Ser	
	275					280					285					290	
5	tcc	aac	agg	ata	ttt	ctt	gaa	gaa	aca	tca	ctc	gta	gct	cgt	cct	ggc	1029
	Ser	Asn	Arg	Ile	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg	Pro	Gly	
					295				300						305		
10	ttg	cgt	ata	gat	gat	att	caa	gaa	cga	atg	gtg	gct	cgt	tta	aac	cat	1077
	Leu	Arg	Ile	Asp	Asp	Ile	Gln	Glu	Arg	Met	Val	Ala	Arg	Leu	Asn	His	
				310					315					320			
15	ttg	ggg	ata	aaa	gtg	aag	agc	att	gaa	gaa	gat	gaa	cat	tgt	cta	ata	1125
	Leu	Gly	Ile	Lys	Val	Lys	Ser	Ile	Glu	Glu	Asp	Glu	His	Cys	Leu	Ile	
		325						330					335				
20	cca	atg	ggg	ggg	cca	ctt	cca	gta	tta	cct	cag	aga	gtc	gtt	gga	atc	1173
	Pro	Met	Gly	Gly	Pro	Leu	Pro	Val	Leu	Pro	Gln	Arg	Val	Val	Gly	Ile	
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	Arg	Thr	Leu	Ala	Ala	Ala	Pro	Val	Val	Ala	Asn	Ala	Ile	Ile	Gln	Tyr	
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	Leu	Gly	Ser	Glu	Arg	Ser	His	Ser	Gly	Asn	Glu	Leu	Ser	Thr	Ala	Val	
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	Trp	Lys	Asp	Leu	Trp	Pro	Ile	Glu	Arg	Arg	Arg	Gln	Arg	Glu	Phe	Phe	
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	Cys	Phe	Gly	Met	Asp	Ile	Leu	Leu	Lys	Leu	Asp	Leu	Pro	Ala	Thr	Arg	
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	Phe	Leu	Ser	Ser	Arg	Leu	Phe	Leu	Pro	Glu	Leu	Ile	Val	Phe	Gly	Leu	
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	Ser	Leu	Phe	Ser	His	Ala	Ser	Asn	Thr	Ser	Arg	Phe	Glu	Ile	Met	Thr	
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Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr  
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Trp Ser Phe His His Asp Asp Leu Thr Glu Ser Gln His Arg Trp Ile

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	Gly Gln Val Ile Gly Ala Arg Ala Val Ile Asp Gly Arg Gly Tyr Ala	
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	Trp Arg Leu Ser His Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp	
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Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln Gln Pro Asp Met Arg Ile  
20 25 30

25

Leu Leu Ile Asp Ala Ala Pro Gln Ala Gly Gly Asn His Thr Trp Ser  
35 40 45

30

Phe His His Asp Asp Leu Thr Glu Ser Gln His Arg Trp Ile Ala Pro  
50 55 60

35

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Thr Arg  
65 70 75 80

40

Arg Arg Lys Leu Asn Ser Gly Tyr Phe Cys Ile Thr Ser Gln Arg Phe  
85 90 95

45

Ala Glu Val Leu Gln Arg Gln Phe Gly Pro His Leu Trp Met Asp Thr  
100 105 110

Ala Val Ala Glu Val Asn Ala Glu Ser Val Arg Leu Lys Lys Gly Gln  
115 120 125

50

Val Ile Gly Ala Arg Ala Val Ile Asp Gly Arg Gly Tyr Ala Ala Asn  
130 135 140

5 Ser Ala Leu Ser Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Arg  
 145 150 155 160  
 Leu Ser His Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr  
 165 170 175  
 10 Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Ser Leu Pro Leu Ser  
 180 185 190  
 15 Pro Thr Arg Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Asn Ala Thr  
 195 200 205  
 20 Leu Asp Pro Glu Cys Ala Arg Gln Asn Ile Cys Asp Tyr Ala Ala Gln  
 210 215 220  
 25 Gln Gly Trp Gln Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu  
 225 230 235 240  
 Pro Ile Thr Leu Ser Gly Asn Ala Asp Ala Phe Trp Gln Gln Arg Pro  
 245 250 255  
 30 Leu Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly  
 260 265 270  
 35 Tyr Ser Leu Pro Leu Ala Val Ala Val Ala Asp Arg Leu Ser Ala Leu  
 275 280 285  
 40 Asp Val Phe Thr Ser Ala Ser Ile His His Ala Ile Thr His Phe Ala  
 290 295 300  
 45 Arg Glu Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met  
 305 310 315 320  
 Leu Phe Leu Ala Gly Pro Ala Asp Ser Arg Trp Arg Val Met Gln Arg  
 325 330 335  
 50 Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys  
 340 345 350

5 Leu Thr Leu Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val  
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10 Pro Val Leu Ala Ala Leu Gln Ala Ile Met Thr Thr  
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                     20                    25                    30

35 Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe  
                     35                    40                    45

40 Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu  
     50                    55                    60

45 Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu  
     65                    70                    75                    80

50 Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val  
                     85                    90                    95

Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln  
                     100                    105                    110

Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser  
                     115                    120                    125

Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe  
 130 135 140  
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 Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu  
 145 150 155 160  
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 Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp  
 165 170 175  
 15  
 Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly  
 180 185 190  
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 Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu  
 195 200 205  
 Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val  
 210 215 220  
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 Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu  
 225 230 235 240  
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 Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala  
 245 250 255  
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 Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser  
 260 265 270  
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 Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro  
 275 280 285  
 Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn  
 290 295 300  
 45  
 Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu  
 305 310 315 320  
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 Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp  
 325 330 335

Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu  
 340 345 350  
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 His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly  
 355 360 365  
 10  
 Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu  
 370 375 380  
 15  
 Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr  
 385 390 395 400  
 20  
 Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His  
 405 410 415  
 25  
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His  
 420 425 430  
 30  
 Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe  
 435 440 445  
 35  
 Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly  
 450 455 460  
 40  
 Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala  
 465 470 475 480  
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 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile  
 485 490  
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 <213> Erwinia uredovora



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 Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His  
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 10  
 Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln  
 35 40 45  
 15  
 Pro Ala Leu Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys  
 50 55 60  
 20  
 Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala  
 65 70 75 80  
 25  
 Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala  
 85 90 95  
 30  
 Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr  
 100 105 110  
 35  
 Ser Gln Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val  
 115 120 125  
 40  
 Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr  
 130 135 140  
 45  
 Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile  
 145 150 155 160  
 50  
 Ala Arg Asp Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro  
 165 170 175  
 Ala Ser Trp Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala  
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 Met Gln Thr Glu His Val Ile Leu Leu  
 1 5  
 50 aat gca cag gga gtt ccc acg ggt acg ctg gaa aag tat gcc gca cac 161  
 Asn Ala Gln Gly Val Pro Thr Gly Thr Leu Glu Lys Tyr Ala Ala His  
 10 15 20 25

	acg gca gac acc cgc tta cat ctc gcg ttc tcc agt tgg ctg ttt aat	209
	Thr Ala Asp Thr Arg Leu His Leu Ala Phe Ser Ser Trp Leu Phe Asn	
	30 35 40	
5	gcc aaa gga caa tta tta gtt acc cgc cgc gca ctg agc aaa aaa gca	257
	Ala Lys Gly Gln Leu Leu Val Thr Arg Arg Ala Leu Ser Lys Lys Ala	
	45 50 55	
10	tgg cct ggc gtg tgg act aac tcg gtt tgt ggg cac cca caa ctg gga	305
	Trp Pro Gly Val Trp Thr Asn Ser Val Cys Gly His Pro Gln Leu Gly	
	60 65 70	
	gaa agc aac gaa gac gca gtg atc cgc cgt tgc cgt tat gag ctt ggc	353
15	Glu Ser Asn Glu Asp Ala Val Ile Arg Arg Cys Arg Tyr Glu Leu Gly	
	75 80 85	
	gtg gaa att acg cct cct gaa tct atc tat cct gac ttt cgc tac cgc	401
	Val Glu Ile Thr Pro Pro Glu Ser Ile Tyr Pro Asp Phe Arg Tyr Arg	
20	90 95 100 105	
	gcc acc gat ccg agt ggc att gtg gaa aat gaa gtg tgt ccg gta ttt	449
	Ala Thr Asp Pro Ser Gly Ile Val Glu Asn Glu Val Cys Pro Val Phe	
	110 115 120	
25	gcc gca cgc acc act agt gcg tta cag atc aat gat gat gaa gtg atg	497
	Ala Ala Arg Thr Thr Ser Ala Leu Gln Ile Asn Asp Asp Glu Val Met	
	125 130 135	
30	gat tat caa tgg tgt gat tta gca gat gta tta cac ggt att gat gcc	545
	Asp Tyr Gln Trp Cys Asp Leu Ala Asp Val Leu His Gly Ile Asp Ala	
	140 145 150	
	acg ccg tgg gcg ttc agt ccg tgg atg gtg atg cag gcg aca aat cgc	593
35	Thr Pro Trp Ala Phe Ser Pro Trp Met Val Met Gln Ala Thr Asn Arg	
	155 160 165	
	gaa gcc aga aaa cga tta tct gca ttt acc cag ctt aaa taa	635
	Glu Ala Arg Lys Arg Leu Ser Ala Phe Thr Gln Leu Lys	
40	170 175 180	
	aaaaaccccg acatttgccg gggtgtgag cataacgtgt cgac	679
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50	<213> Escherichia coli	

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5 Met Gln Thr Glu His Val Ile Leu Leu Asn Ala Gln Gly Val Pro Thr  
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10 Gly Thr Leu Glu Lys Tyr Ala Ala His Thr Ala Asp Thr Arg Leu His  
 20 25 30

15 Leu Ala Phe Ser Ser Trp Leu Phe Asn Ala Lys Gly Gln Leu Leu Val  
 35 40 45

20 Thr Arg Arg Ala Leu Ser Lys Lys Ala Trp Pro Gly Val Trp Thr Asn  
 50 55 60

25 Ser Val Cys Gly His Pro Gln Leu Gly Glu Ser Asn Glu Asp Ala Val  
 65 70 75 80

30 Ile Arg Arg Cys Arg Tyr Glu Leu Gly Val Glu Ile Thr Pro Pro Glu  
 85 90 95

35 Ser Ile Tyr Pro Asp Phe Arg Tyr Arg Ala Thr Asp Pro Ser Gly Ile  
 100 105 110

40 Val Glu Asn Glu Val Cys Pro Val Phe Ala Ala Arg Thr Thr Ser Ala  
 115 120 125

45 Leu Gln Ile Asn Asp Asp Glu Val Met Asp Tyr Gln Trp Cys Asp Leu  
 130 135 140

50 Ala Asp Val Leu His Gly Ile Asp Ala Thr Pro Trp Ala Phe Ser Pro  
 145 150 155 160

45 Trp Met Val Met Gln Ala Thr Asn Arg Glu Ala Arg Lys Arg Leu Ser  
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50 Ala Phe Thr Gln Leu Lys  
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tttttaagct ttcacttttt tcttgtaacc aa  
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32

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&lt;213&gt; Archaeoglobus fulgidus

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&lt;221&gt; CDS

&lt;222&gt; (3)..(956)

&lt;223&gt;

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&lt;400&gt; 34

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cc atg gtg aag gag gaa ata gcg aaa agg gcc gaa ata atc aac aaa 47  
 Met Val Lys Glu Glu Ile Ala Lys Arg Ala Glu Ile Ile Asn Lys  
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25

gcc att gaa gag ctt ctg ccc gaa agg gag ccg att gga ctc tac aaa 95  
 Ala Ile Glu Glu Leu Leu Pro Glu Arg Glu Pro Ile Gly Leu Tyr Lys  
 20 25 30

30

gcc gca agg cat ctg atc aaa gca ggt ggc aag agg cta agg cct gta 143  
 Ala Ala Arg His Leu Ile Lys Ala Gly Gly Lys Arg Leu Arg Pro Val  
 35 40 45

35

ata agc ctc tta gca gtc gaa gcc ctt ggg aaa gac tac aga aag att 191  
 Ile Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile  
 50 55 60

40

atc ccg gct gct gtc agc att gaa aca atc cac aac ttc acc ctc gtg 239  
 Ile Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val  
 65 70 75

cat gac gac ata atg gac agg gac gag atg agg agg gga gtt ccg acg 287  
 His Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr  
 80 85 90 95

45

gta cac agg gtt tat ggg gaa gcg acg gcc att tta gca ggc gac aca 335  
 Val His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr  
 100 105 110

ctc ttt gct gaa gcc ttc aag ctg ctg aca aag tgc gat gtt gag agc 383  
 Leu Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser  
 115 120 125

50

gag gga atc aga aaa gct aca gaa atg ctt tcg gac gtt tgc ata aaa 431  
 Glu Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys  
 130 135 140

ata tgc gag ggg cag tac tac gac atg agc ttt gag aaa aag gag agc 479  
 Ile Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser  
 145 150 155  
 5 gtt tcc gag gag gag tat ctc agg atg gtc gag ctg aag acc gga gtg 527  
 Val Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val  
 160 165 170 175  
 10 ctg att gca gct tct gca gca tta cct gcg gtg ctt ttt ggg gag agc 575  
 Leu Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser  
 180 185 190  
 15 gag gaa att gta aag gcg ctg tgg gac tac gga gtt ctt agc ggt att 623  
 Glu Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile  
 195 200 205  
 20 ggc ttc cag atc cag gac gac ctg ctt gac ctg act gag gag acc gga 671  
 Gly Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly  
 210 215 220  
 25 aag gac tgg gga agc gac ctg ctt aaa ggg aag aaa acc ctg att gtc 719  
 Lys Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val  
 225 230 235  
 30 ata aag gcg ttc gaa aag gga gtg aag cta aag acg ttt gga aag gaa 767  
 Ile Lys Ala Phe Glu Lys Gly Val Lys Leu Lys Thr Phe Gly Lys Glu  
 240 245 250 255  
 35 aag gcg gac gtc tct gag att aga gat gat atc gaa aag tta aga gag 815  
 Lys Ala Asp Val Ser Glu Ile Arg Asp Asp Ile Glu Lys Leu Arg Glu  
 260 265 270  
 40 tgt ggt gcg att gat tac gct gcc agc atg gca aga aag atg gct gaa 863  
 Cys Gly Ala Ile Asp Tyr Ala Ala Ser Met Ala Arg Lys Met Ala Glu  
 275 280 285  
 45 gag gcg aaa aga aag ctc gaa gtt ctg cct gaa agc aaa gcc aag gaa 911  
 Glu Ala Lys Arg Lys Leu Glu Val Leu Pro Glu Ser Lys Ala Lys Glu  
 290 295 300  
 50 aca ctg ctg gaa ctt acc gac ttc ttg gtt aca aga aaa aag tga 956  
 Thr Leu Leu Glu Leu Thr Asp Phe Leu Val Thr Arg Lys Lys  
 305 310 315  
 aagctt 962  
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&lt;212&gt; PRT

&lt;213&gt; Archaeoglobus fulgidus

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&lt;400&gt; 35

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Ile Glu Glu Leu Leu Pro Glu Arg Glu Pro Ile Gly Leu Tyr Lys Ala  
 20 25 30

15

Ala Arg His Leu Ile Lys Ala Gly Gly Lys Arg Leu Arg Pro Val Ile  
 35 40 45

20

Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile Ile  
 50 55 60

25

Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val His  
 65 70 75 80

30

Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr Val  
 85 90 95

35

His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr Leu  
 100 105 110

Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser Glu  
 115 120 125

40

Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys Ile  
 130 135 140

45

Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser Val  
 145 150 155 160

50

Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val Leu  
 165 170 175

58

Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser Glu  
 180 185 190

5 Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile Gly  
 195 200 205

10 Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly Lys  
 210 215 220

15 Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val Ile  
 225 230 235 240

Lys Ala Phe Glu Lys Gly Val Lys Leu Lys Thr Phe Gly Lys Glu Lys  
 245 250 255

20 Ala Asp Val Ser Glu Ile Arg Asp Asp Ile Glu Lys Leu Arg Glu Cys  
 260 265 270

25 Gly Ala Ile Asp Tyr Ala Ala Ser Met Ala Arg Lys Met Ala Glu Glu  
 275 280 285

30 Ala Lys Arg Lys Leu Glu Val Leu Pro Glu Ser Lys Ala Lys Glu Thr  
 290 295 300

35 Leu Leu Glu Leu Thr Asp Phe Leu Val Thr Arg Lys Lys  
 305 310 315

<210> 36

40 <211> 1293

<212> DNA

<213> Archaeoglobus fulgidus

45 <220>

<221> CDS

50 <222> (206)..(1159)

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 10 gggggcaggg atggctatat ttctgggagc gaactccggg cgaggatcta gttgtaggga 180  
 gggattcatg acaccacaaa cagcc atg gtg aag gag gaa ata gcg aaa agg 232  
 Met Val Lys Glu Glu Ile Ala Lys Arg  
 1 5  
 15 gcc gaa ata atc aac aaa gcc att gaa gag ctt ctg ccc gaa agg gag 280  
 Ala Glu Ile Ile Asn Lys Ala Ile Glu Glu Leu Leu Pro Glu Arg Glu  
 10 15 20 25  
 20 ccg att gga ctc tac aaa gcc gca agg cat ctg atc aaa gca ggt gcc 328  
 Pro Ile Gly Leu Tyr Lys Ala Ala Arg His Leu Ile Lys Ala Gly Gly  
 30 35 40  
 aag agg cta agg cct gta ata agc ctc tta gca gtc gaa gcc ctt ggg 376  
 25 Lys Arg Leu Arg Pro Val Ile Ser Leu Leu Ala Val Glu Ala Leu Gly  
 45 50 55  
 aaa gac tac aga aag att atc ccg gct gct gtc agc att gaa aca atc 424  
 30 Lys Asp Tyr Arg Lys Ile Ile Pro Ala Ala Val Ser Ile Glu Thr Ile  
 60 65 70  
 cac aac ttc acc ctc gfg cat gac gac ata atg gac agg gac gag atg 472  
 His Asn Phe Thr Leu Val His Asp Asp Ile Met Asp Arg Asp Glu Met  
 75 80 85  
 35 agg agg gga gtt ccg acg gta cac agg gtt tat ggg gaa gcg acg gcc 520  
 Arg Arg Gly Val Pro Thr Val His Arg Val Tyr Gly Glu Ala Thr Ala  
 90 95 100 105  
 40 att tta gca ggc gac aca ctc ttt gct gaa gcc ttc aag ctg ctg aca 568  
 Ile Leu Ala Gly Asp Thr Leu Phe Ala Glu Ala Phe Lys Leu Leu Thr  
 110 115 120  
 aag tgc gat gtt gag agc gag gga atc aga aaa gct aca gaa atg ctt 616  
 45 Lys Cys Asp Val Glu Ser Glu Gly Ile Arg Lys Ala Thr Glu Met Leu  
 125 130 135  
 tcg gac gtt tgc ata aaa ata tgc gag ggg cag tac tac gac atg agc 664  
 Ser Asp Val Cys Ile Lys Ile Cys Glu Gly Gln Tyr Tyr Asp Met Ser  
 50 140 145 150  
 ttt gag aaa aag gag agc gtt tcc gag gag gag tat ctc agg atg gtc 712

## 60

Phe Glu Lys Lys Glu Ser Val Ser Glu Glu Glu Tyr Leu Arg Met Val  
 155 160 165

5 gag ctg aag acc gga gtg ctg att gca gct tct gca gca tta cct gcg 760  
 Glu Leu Lys Thr Gly Val Leu Ile Ala Ala Ser Ala Ala Leu Pro Ala  
 170 175 180 185

10 gtg ctt ttt ggg gag agc gag gaa att gta aag gcg ctg tgg gac tac 808  
 Val Leu Phe Gly Glu Ser Glu Glu Ile Val Lys Ala Leu Trp Asp Tyr  
 190 195 200

15 gga gtt ctt agc ggt att ggc ttc cag atc cag gac gac ctg ctt gac 856  
 Gly Val Leu Ser Gly Ile Gly Phe Gln Ile Gln Asp Asp Leu Leu Asp  
 205 210 215

ctg act gag gag acc gga aag gac tgg gga agc gac ctg ctt aaa ggg 904  
 Leu Thr Glu Glu Thr Gly Lys Asp Trp Gly Ser Asp Leu Leu Lys Gly  
 220 225 230

20 aag aaa acc ctg att gtc ata aag gcg ttc gaa aag gga gtg aag cta 952  
 Lys Lys Thr Leu Ile Val Ile Lys Ala Phe Glu Lys Gly Val Lys Leu  
 235 240 245

25 aag acg ttt gga aag gaa aag gcg gac gtc tct gag att aga gat gat 1000  
 Lys Thr Phe Gly Lys Glu Lys Ala Asp Val Ser Glu Ile Arg Asp Asp  
 250 255 260 265

30 atc gaa aag tta aga gag tgt ggt gcg att gat tac gct gcc agc atg 1048  
 Ile Glu Lys Leu Arg Glu Cys Gly Ala Ile Asp Tyr Ala Ala Ser Met  
 270 275 280

35 gca aga aag atg gct gaa gag gcg aag aga aag ctc gaa gtt ctg cct 1096  
 Ala Arg Lys Met Ala Glu Glu Ala Lys Arg Lys Leu Glu Val Leu Pro  
 285 290 295

gaa agc aaa gcc aag gaa aca ctg ctg gaa ctt acc gac ttc ttg gtt 1144  
 Glu Ser Lys Ala Lys Glu Thr Leu Leu Glu Leu Thr Asp Phe Leu Val  
 300 305 310

40 aca aga aaa aag tga aagcttcaat tgcattgctct agatgatcaa agaattcctg 1199  
 Thr Arg Lys Lys  
 315

45 gcctagtcta taggaggttt tgaaaagaaa ggagcaataa tcattttctt gttctatcaa 1259  
 gaggggtgcta ttgctccttt ctttttttct cgag 1293

<210> 37  
 <211> 317

&lt;212&gt; PRT

<213> *Archaeoglobus fulgidus*

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&lt;400&gt; 37

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15 Ile Glu Glu Leu Leu Pro Glu Arg Glu Pro Ile Gly Leu Tyr Lys Ala  
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Ala Arg His Leu Ile Lys Ala Gly Gly Lys Arg Leu Arg Pro Val Ile  
35 40 45

20 Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile Ile  
50 55 60

25 Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val His  
65 70 75 80

30 Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr Val  
85 90 95

35 His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr Leu  
100 105 110

Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser Glu  
115 120 125

40 Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys Ile  
130 135 140

45 Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser Val  
145 150 155 160

50 Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val Leu  
165 170 175

## 62

Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser Glu  
180 185 190

5 Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile Gly  
195 200 205

10 Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly Lys  
210 215 220

15 Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val Ile  
225 230 235 240

Lys Ala Phe Glu Lys Gly Val Lys Leu Lys Thr Phe Gly Lys Glu Lys  
245 250 255

20 Ala Asp Val Ser Glu Ile Arg Asp Asp Ile Glu Lys Leu Arg Glu Cys  
260 265 270

25 Gly Ala Ile Asp Tyr Ala Ala Ser Met Ala Arg Lys Met Ala Glu Glu  
275 280 285

30 Ala Lys Arg Lys Leu Glu Val Leu Pro Glu Ser Lys Ala Lys Glu Thr  
290 295 300

35 Leu Leu Glu Leu Thr Asp Phe Leu Val Thr Arg Lys Lys  
305 310 315

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&lt;211&gt; 38

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35 <211> 647

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

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&lt;220&gt;

45 <221> Promoter

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&lt;223&gt;

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 5 tctctggctg atcttttctg tacagattca tatactctga gagacgatat cattgattat 180  
 ttgagcttct tttgaactat ttcgtgtaat ttgggatgag agctctatgt atgtgtgtaa 240  
 10 actttgaaga caacaagaaa ggtaacaagt gagggaggga tgactccatg tcaaaataga 300  
 tgtcataaga ggcccatcaa taagtgcttg agccpattag ctagcccagt aactaccaga 360  
 ttgtgagatg gatgtgtgaa cagttttttt ttgtatgtag gactgaaatg tgaacaacag 420  
 15 gcgcatgaaa ggctaaatta ggacaatgat aagcagaaat aactatcct ctctaact 480  
 tggcctcaca ttgcccttca cacaatccac acacatccaa tcacaacctc atcatatc 540  
 20 tcccgctaata ctttttttct ttgatctttt tttttttgtt tattattttt ttgactttga 600  
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agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagttagga 180

ccaaacatta tctacaaaca aagacttttc tcctaacttg tgattccttc ttaaacccta 240

45 ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta 300

atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360

50 tatatatctc tttcttctta tttcccaaata taacagacaa aagtagaata ttggctttta 420

acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgca 480

aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540  
 ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600  
 5 tcacttagtt ttcatcaact tctgaactta cttttcatgg attaggcaat actttccatt, 660  
 tttagtaact caagtgagacc ctttacttct tcaactccat ctctctcttt ctatttcact 720  
 10 tctttcttct cattatatct cttgtcctct ccaccaaata tcttcaacaa aaagctt 777

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 cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96  
 40 Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala  
 20 25 30  
 ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc 144  
 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu  
 35 40 45  
 45 tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg 192  
 Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu  
 50 55 60  
 50 ttg att ggc agc ttg att ctg ctc aga gca ttt ctg cac acc ggg ctg 240  
 Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu  
 65 70 75 80

	ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat	288
	Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His	
	85 90 95	
5	ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca	336
	Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala	
	100 105 110	
10	ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac ctg	384
	Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu	
	115 120 125	
15	gca ccg gag acg ttc cag gat cct gac tac caa cgt tgc acc aat aac	432
	Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn	
	130 135 140	
20	aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg	480
	Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met	
	145 150 155 160	
25	cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc	528
	Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu	
	165 170 175	
30	aac ggt tct gat ctc cct gct cag atc atg cat ctg ctg ttg ttc agc	576
	Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser	
	180 185 190	
35	gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc	624
	Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr	
	195 200 205	
40	tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg	672
	Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr	
	210 215 220	
45	cgc agc ctg gct ttg cat cca gcc ctc tct ttc gca gct tgt tac aac	720
	Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn	
	225 230 235 240	
50	ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt	768
	Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe	
	245 250 255	
55	cag ctg cca caa ctt cga aat gaa tca ttc act tga	804
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&lt;211&gt; 267

&lt;212&gt; PRT

5 &lt;213&gt; Synechococcus WH8102

&lt;400&gt; 47

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Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His  
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Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala  
 20 25 30

20

Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu  
 35 40 45

25

Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu  
 50 55 60

30

Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu  
 65 70 75 80

Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His  
 85 90 95

35

Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala  
 100 105 110

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Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu  
 115 120 125

45

Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn  
 130 135 140

Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met  
 145 150 155 160

50

Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu  
 165 170 175

Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser  
 180 185 190  
 5  
 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr  
 195 200 205  
 10  
 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr  
 210 215 220  
 15  
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn  
 225 230 235 240  
 20  
 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe  
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 cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96

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				20					25					30			
5	ctc	aaa	ggg	ttg	gct	ctg	gct	ggg	ctg	att	gga	tca	gcc	ttg	ctg	ctc	144
	Leu	Lys	Gly	Leu	Ala	Leu	Ala	Gly	Leu	Ile	Gly	Ser	Ala	Trp	Leu	Leu	
			35					40					45				
10	tcc	ctg	ggc	ctg	agc	tac	acc	ctg	cca	ctt	gat	cag	acg	cct	ggg	ctg	192
	Ser	Leu	Gly	Leu	Ser	Tyr	Thr	Leu	Pro	Leu	Asp	Gln	Thr	Pro	Gly	Leu	
		50					55					60					
15	ttg	att	ggc	agc	ttg	att	ctg	tgg	cag	acc	ttt	ctg	cac	acc	ggg	ctg	240
	Leu	Ile	Gly	Ser	Leu	Ile	Leu	Trp	Gln	Thr	Phe	Leu	His	Thr	Gly	Leu	
	65					70					75				80		
	ttc	atc	gtt	gcc	cac	gat	tcc	atg	cac	gcc	agt	ctg	gtt	ccg	ggg	cat	288
	Phe	Ile	Val	Ala	His	Asp	Ser	Met	His	Ala	Ser	Leu	Val	Pro	Gly	His	
				85					90						95		
20	ccc	gga	ttg	aac	cgc	tgg	atc	ggc	aaa	gtg	tat	ttg	ttg	gtg	tat	gca	336
	Pro	Gly	Leu	Asn	Arg	Trp	Ile	Gly	Lys	Val	Tyr	Leu	Leu	Val	Tyr	Ala	
				100					105						110		
25	ggc	ttg	tct	tat	gag	cgt	tgt	tcc	cgc	aac	cac	aga	cgt	cat	cac	ctg	384
	Gly	Leu	Ser	Tyr	Glu	Arg	Cys	Ser	Arg	Asn	His	Arg	Arg	His	His	Leu	
			115					120					125				
30	gca	ccg	gag	acg	ttc	cag	gat	cct	gac	tac	caa	cgt	tgc	acc	aat	aac	432
	Ala	Pro	Glu	Thr	Phe	Gln	Asp	Pro	Asp	Tyr	Gln	Arg	Cys	Thr	Asn	Asn	
		130					135					140					
35	aac	atc	cta	gat	tgg	tat	gtt	cac	ttc	atg	ggc	aac	tat	ctg	ggc	atg	480
	Asn	Ile	Leu	Asp	Trp	Tyr	Val	His	Phe	Met	Gly	Asn	Tyr	Leu	Gly	Met	
	145					150					155				160		
	cgg	caa	ctg	tta	aat	cta	agc	tgt	ctt	tgg	ctg	gcg	cta	atc	att	ctc	528
	Arg	Gln	Leu	Leu	Asn	Leu	Ser	Cys	Leu	Trp	Leu	Ala	Leu	Ile	Ile	Leu	
					165					170					175		
40	aac	ggg	tct	gat	ctc	cct	gct	cag	atc	atg	cat	ctg	ctg	ttg	ttc	agc	576
	Asn	Gly	Ser	Asp	Leu	Pro	Ala	Gln	Ile	Met	His	Leu	Leu	Leu	Phe	Ser	
				180					185						190		
45	gtt	ctg	ccg	ttg	atc	atc	agt	tcc	tgt	caa	ttg	ttt	cta	gtg	gga	acc	624
	Val	Leu	Pro	Leu	Ile	Ile	Ser	Ser	Cys	Gln	Leu	Phe	Leu	Val	Gly	Thr	
			195					200					205				
50	tgg	tta	ccc	cac	cga	cgt	ggg	gcc	acg	aca	cga	ccg	ggc	gtg	aca	acg	672
	Trp	Leu	Pro	His	Arg	Arg	Gly	Ala	Thr	Thr	Arg	Pro	Gly	Val	Thr	Thr	
		210					215					220					
	cgc	agc	ctg	gct	ttg	cat	cca	gcc	ctc	tct	ttc	gca	gct	tgt	tac	aac	720

72

	Arg Ser Leu Ala	Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn	
	225	230	235 240
5	ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe	245	250 255 768
10	cag ctg cca caa ctt cga aat gaa tca ttc act tga Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr	260	265 804
15	<210> 49 <211> 267 <212> PRT <213> Artificial variant		
20	<400> 49		
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35	Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu 35 40 45		
40	Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu 50 55 60		
45	Leu Ile Gly Ser Leu Ile Leu Trp Gln Thr Phe Leu His Thr Gly Leu 65 70 75 80		
50	Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His 85 90 95		
	Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala 100 105 110		



Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu  
 115 120 125

5 Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn  
 130 135 140

10 Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met  
 145 150 155 160

Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu  
 165 170 175

15 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser  
 180 185 190

20 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr  
 195 200 205

25 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr  
 210 215 220

30 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn  
 225 230 235 240

35 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe  
 245 250 255

Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr  
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40 <210> 50  
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15	cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc	96
	Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala	
	20 25 30	
20	ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc	144
	Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu	
	35 40 45	
25	tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg	192
	Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu	
	50 55 60	
30	ttg att ggc agc ttg att ctg ctc aga gca ttt ctg cac acc ggg ctg	240
	Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu	
	65 70 75 80	
35	ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat	288
	Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His	
	85 90 95	
40	ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca	336
	Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala	
	100 105 110	
45	ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac gga	384
	Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Gly	
	115 120 125	
50	cat cct ggt act gat tta gat cct gac tac caa cgt tgc acc aat aac	432
	His Pro Gly Thr Asp Leu Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn	
	130 135 140	
55	aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg	480
	Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met	
	145 150 155 160	
60	cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc	528
	Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu	
	165 170 175	

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 180 185 190

5 gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc 624  
 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr  
 195 200 205

10 tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg 672  
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 210 215 220

15 cgc agc ctg gct ttg cat cca gcc ctc tct ttc gca gct tgt tac aac 720  
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn  
 225 230 235 240

20 ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt 768  
 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe  
 245 250 255

cag ctg cca caa ctt cga aat gaa tca ttc act tga 804  
 Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr  
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<210> 51

<211> 267

30 <212> PRT

<213> Artificial variant

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<400> 51

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Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala  
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Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu  
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50

Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu  
 50 55 60

5 Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu  
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 Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His  
 85 90 95  
 10 Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala  
 100 105 110  
 15 Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Gly  
 115 120 125  
 20 His Pro Gly Thr Asp Leu Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn  
 130 135 140  
 25 Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met  
 145 150 155 160  
 Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu  
 165 170 175  
 30 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser  
 180 185 190  
 35 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr  
 195 200 205  
 40 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr  
 210 215 220  
 45 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn  
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 ctt tat att gat ata tcc caa ttc aag ttt tgg atg ttg tta ccg ctc 96  
 Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu  
 30 20 25 30  
 ata ttt tgg caa aca ttt tta tat acg gga tta ttt att aca gct cat 144  
 Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
 35 35 40 45  
 gat gcc atg cat ggg gta gtt ttt ccc aaa aat ccc aaa atc aac cat 192  
 Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His  
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 40 ttc att ggc tca ttg tgc ctg ttt ctt tat ggt ctt tta cct tat caa 240  
 Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln  
 65 70 75 80  
 aaa ctt tta aaa aag cat tgg cta cat cac cat aat cca gcc agt gaa 288  
 45 Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu  
 85 90 95  
 aca gat cca gat ttt cac aac ggg aag cag aaa aac ttt ttt gct tgg 336  
 Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp  
 50 100 105 110  
 tat tta tat ttt atg aag cgt tac tgg agt tgg tta caa att atc aca 384

	Tyr	Leu	Tyr	Phe	Met	Lys	Arg	Tyr	Trp	Ser	Trp	Leu	Gln	Ile	Ile	Thr	
		115						120					125				
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	Leu	Met	Ile	Ile	Tyr	Asn	Leu	Leu	Lys	Tyr	Ile	Trp	His	Phe	Pro	Glu	
		130					135					140					
10	gat	aat	atg	act	tat	ttt	tgg	gta	gtt	ccc	tca	att	tta	agt	tct	tta	480
	Asp	Asn	Met	Thr	Tyr	Phe	Trp	Val	Val	Pro	Ser	Ile	Leu	Ser	Ser	Leu	
		145					150				155					160	
15	caa	tta	ttt	tat	ttt	gga	act	ttt	cta	ccc	cac	agt	gag	cct	gta	gaa	528
	Gln	Leu	Phe	Tyr	Phe	Gly	Thr	Phe	Leu	Pro	His	Ser	Glu	Pro	Val	Glu	
					165					170					175		
	ggt	tat	aaa	gag	cct	cat	cgt	tcc	caa	act	att	agc	cgt	ccc	att	tgg	576
	Gly	Tyr	Lys	Glu	Pro	His	Arg	Ser	Gln	Thr	Ile	Ser	Arg	Pro	Ile	Trp	
			180						185					190			
20	tgg	tca	ttt	ata	act	tgt	tac	cat	ttt	ggt	tat	cat	tac	gaa	cat	cat	624
	Trp	Ser	Phe	Ile	Thr	Cys	Tyr	His	Phe	Gly	Tyr	His	Tyr	Glu	His	His	
			195					200					205				
25	gaa	tac	ccc	cat	gtt	cct	tgg	tgg	caa	tta	cca	gaa	att	tat	aaa	atg	672
	Glu	Tyr	Pro	His	Val	Pro	Trp	Trp	Gln	Leu	Pro	Glu	Ile	Tyr	Lys	Met	
		210					215					220					
30	tct	aaa	tca	aat	ttg	tga											690
	Ser	Lys	Ser	Asn	Leu												
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	1				5					10					15		
50	Leu	Tyr	Ile	Asp	Ile	Ser	Gln	Phe	Lys	Phe	Trp	Met	Leu	Leu	Pro	Leu	
			20						25						30		

Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
 35 40 45

5 Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His  
 50 55 60

10 Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln  
 65 70 75 80

15 Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu  
 85 90 95

Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp  
 100 105 110

20 Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr  
 115 120 125

25 Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu  
 130 135 140

30 Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu  
 145 150 155 160

35 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu  
 165 170 175

Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp  
 180 185 190

40 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His  
 195 200 205

45 Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met  
 210 215 220

50 Ser Lys Ser Asn Leu  
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<213> Nostoc punctiforme ATCC 29133

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<223>

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<400> 56

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1					5					10					15

qca aaa ctg act cca gta ctg aga agt aaa tct cag ttt aag ggg ctt , 97

Ala	Lys	Leu	Thr	Pro	Val	Leu	Arg	Ser	Lys	Ser	Gln	Phe	Lys	Gly	Leu
				20					25					30	

25

ttc att gct att gtc att gtt agc gca tgg gtc att' agc ctg agt tta 145

Phe Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu  
35 40 45

30

tta ctt tcc ctt gac atc tca aag cta aaa ttt tgg atg tta ttg cct 193

Leu Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro  
50 55 60

35

gtt ata cta tgg caa aca ttt tta tat acg gga tta ttt att aca tct 241

Val Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser  
65 70 75

40

cat qat qcc atg cat ggc gta gta ttt ccc caa aac acc aag att aat 289

His	Asp	Ala	Met	His	Gly	Val	Val	Phe	Pro	Gln	Asn	Thr	Lys	Ile	Asn
80					85					90					95

cat ttg att gga aca ttg acc cta tcc ctt tat ggt ctt tta cca tat 337

His Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr  
100 105 110

45

caa aaa cta ttg aaa aaa cat tgg tta cac cac cac aat cca gca agc 385

Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser  
115 120 125

50

tca ata gac ccg gat ttt cac aat ggt aaa cac caa agt ttc ttt gct 433

Ser Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala  
130 135 140

	tgg tat ttt cat ttt atg aaa ggt tac tgg agt tgg ggg caa ata att	481
	Trp Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile	
	145                      150                      155	
5	gcg ttg act att att tat aac ttt gct aaa tac ata ctc cat atc cca	529
	Ala Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro	
	160                      165                      170                      175	
10	agt gat aat cta act tac ttt tgg gtg cta ccc tcg ctt tta agt tca	577
	Ser Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser	
	180                      185                      190	
15	tta caa tta ttc tat ttt ggt act ttt tta ccc cat agt gaa cca ata	625
	Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile	
	195                      200                      205	
20	ggg ggt tat gtt cag cct cat tgt gcc caa aca att agc cgt cct att	673
	Gly Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile	
	210                      215                      220	
25	tgg tgg tca ttt atc acg tgc tat cat ttt ggc tac cac gag gaa cat	721
	Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His	
	225                      230                      235	
30	cac gaa tat cct cat att tct tgg tgg cag tta cca gaa att tac aaa	769
	His Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys	
	240                      245                      250                      255	
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	Ala Lys	
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	20                      25                      30	

	Ile	Ala	Ile	Val	Ile	Val	Ser	Ala	Trp	Val	Ile	Ser	Leu	Ser	Leu	Leu	
				35					40						45		
5																	
	Leu	Ser	Leu	Asp	Ile	Ser	Lys	Leu	Lys	Phe	Trp	Met	Leu	Leu	Pro	Val	
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10																	
	Ile	Leu	Trp	Gln	Thr	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Ser	His	
	65					70					75					80	
15																	
	Asp	Ala	Met	His	Gly	Val	Val	Phe	Pro	Gln	Asn	Thr	Lys	Ile	Asn	His	
					85					90					95		
20																	
	Leu	Ile	Gly	Thr	Leu	Thr	Leu	Ser	Leu	Tyr	Gly	Leu	Leu	Pro	Tyr	Gln	
				100					105						110		
25																	
	Lys	Leu	Leu	Lys	Lys	His	Trp	Leu	His	His	His	Asn	Pro	Ala	Ser	Ser	
			115					120					125				
30																	
	Ile	Asp	Pro	Asp	Phe	His	Asn	Gly	Lys	His	Gln	Ser	Phe	Phe	Ala	Trp	
		130					135					140					
35																	
	Tyr	Phe	His	Phe	Met	Lys	Gly	Tyr	Trp	Ser	Trp	Gly	Gln	Ile	Ile	Ala	
	145					150					155					160	
40																	
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					165					170					175		
45																	
	Asp	Asn	Leu	Thr	Tyr	Phe	Trp	Val	Leu	Pro	Ser	Leu	Leu	Ser	Ser	Leu	
				180					185					190			
50																	
	Gln	Leu	Phe	Tyr	Phe	Gly	Thr	Phe	Leu	Pro	His	Ser	Glu	Pro	Ile	Gly	
		195					200						205				
55																	
	Gly	Tyr	Val	Gln	Pro	His	Cys	Ala	Gln	Thr	Ile	Ser	Arg	Pro	Ile	Trp	
		210					215										

Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala  
245 250 255

5

Lys

10

&lt;210&gt; 58

&lt;211&gt; 26

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&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

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&lt;220&gt;

&lt;221&gt; Primer

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&lt;222&gt; (1)..(26)

&lt;223&gt;

30

&lt;400&gt; 58

gtcgac<sup>c</sup>ctg ctttaatgag atatgc

26

35

&lt;210&gt; 59

&lt;211&gt; 27

&lt;212&gt; DNA

40

&lt;213&gt; Artificial sequence

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&lt;220&gt;

&lt;221&gt; Primer

&lt;222&gt; (1)..(27)

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&lt;223&gt;

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&lt;212&gt; DNA

40 <213> Arabidopsis thaliana

&lt;220&gt;

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5 gaatttctct ggctgatctt ttctgtacag attcatatat ctgcagagac gatatcattg 180  
attatttgag cttcttttga actatttcgt gtaatttggg atgagagctc tatgtatgtg 240  
10 tgtaaacttt gaagacaaca agaaaggtaa caagtgaggg agggatgact ccatgtcaaa 300  
atagatgtca taagaggccc atcaataagt gcttgagccc attagctagc ccagtaacta 360  
ccagattgtg agatggatgt gtgaacagtt ttttttttga tgtaggactg aaatgtgaac 420  
15 aacaggcgca tgaaaggcta aattaggaca atgataagca gaaataactt atcctctcta 480  
acacttgccc tcacattgcc cttcacacaa tccacacaca tccaatcaca acctcatcat 540  
20 atatctcccg ctaatctttt tttctttgat cttttttttt ttgcttatta tttttttgac 600  
tttgatctcc catcagttca tcttcttctt cttcttctga tcaaccaagc tt 652  
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<220>

<221> Primer

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<210> 66

<211> 1773

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<212> DNA

<213> Petunia hybrida

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<220>

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<223>

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45

catttggtta ctctctgctg tggtagttgg catatccaca ttgtctcctt ccacttttat 180

gacaattacg tgaaagttat gggttgtttt gtctattttt gtcgaggcct ttcttttcct 240

50

tccaggttgt tgaagatggt ccaattcgat tagaataatg ttttgagctt tagcatattc 300

tctctcgttt acacgattat agtaataatg atataggatg acagaagttg acacataaat 360



tttttattct ctccatttac tttaatccaa atctcaccta ccctaaactt ctttaatatg 420  
 tattcaatag tctatccgag taaattgtaa atttaacaac cattgataat attgacacct 480  
 5 actaacatat actagtaaag agaattattaa catggcacat ataatttgat gcaaaatgag 540  
 tatgatgaaa tttaaaccba aaatctcttg attttgacag tgtcaccttg acttggtaac 600  
 10 taataagtca tgtttttagtg gcagaaagac aaactcatcc accaactgta tagcaataaa 660  
 aaatagaaga atcttcctga ggcaaagttt tggaaaaatt aagagtggct gagatttaat 720  
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45

gcgcgatgctc tagattacga attggttact gaattgt

37

<210> 69

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<211> 819

<212> DNA

&lt;213&gt; Nostoc punctiforme ATCC 29133

5 &lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5)..(802)

10

&lt;223&gt;

15

&lt;400&gt; .69

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           1                  5                  10                  15

20

gtt gca ata gag caa tta agt gct aaa gaa gat act gtt tgg ggg ctg 97  
 Val Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu  
                   20                  25                  30

25

gtg att gtc ata gta att att agt ctt tgg gta gct agt ttg gct ttt 145  
 Val Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe  
                   35                  40                  45

30

tta cta gct att aat tat gcc aaa gtc cca att tgg ttg ata cct att 193  
 Leu Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile  
                   50                  55                  60

35

gca ata gtt tgg caa atg ttc ctt tat aca ggg cta ttt att act gca 241  
 Ala Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala  
                   65                  70                  75

cat gat gct atg cat ggg tca gtt tat cgt aaa aat ccc aaa att aat 289  
 His Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn  
 80                  85                  90                  95

40

aat ttt atc ggt tca cta gct gta gcg ctt tac gct gtg ttt cca tat 337  
 Asn Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr  
                   100                  105                  110

45

caa cag atg tta aag aat cat tgc tta cat cat cgt cat cct gct agc 385  
 Gln Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser  
                   115                  120                  125

50

gaa gtt gac cca gat ttt cat gat ggt aag aga aca aac gct att ttc 433  
 Glu Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe  
                   130                  135                  140

tgg tat ctc cat ttc atg ata gaa tac tcc agt tgg caa cag tta ata 481

Trp Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile  
 145 150 155

5 gta cta act atc cta ttt aat tta gct aaa tac gtt ttg cac atc cat 529  
 Val Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His  
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10 caa ata aat ctc atc tta ttt tgg agt att cct cca att tta agt tcc 577  
 Gln Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser  
 180 185 190

15 att caa ctg ttt tat ttc gga aca ttt ttg cct cat cga gaa ccc aag 625  
 Ile Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys  
 195 200 205

aaa gga tat gtt tat ccc cat tgc agc caa aca ata aaa ttg cca act 673  
 Lys Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr  
 210 215 220

20 ttt ttg tca ttt atc gct tgc tac cac ttt ggt tat cat gaa gaa cat 721  
 Phe Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His  
 225 230 235

25 cat gag tat ccc cat gta cct tgg tgg caa ctt cca tct gta tat aag 769  
 His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys  
 240 245 250 255

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35 <211> 266

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5 Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala  
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10 Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
 65 70 75 80

15 Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn  
 85 90 95

Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln  
 100 105 110

20 Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser Glu  
 115 120 125

25 Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp  
 130 135 140

30 Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val  
 145 150 155 160

35 Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln  
 165 170 175

Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile  
 180 185 190

40 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys  
 195 200 205

45 Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe  
 210 215 220

50 Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His  
 225 230 235 240

Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln  
245 250 255

5 Arg Val Phe Asn Asn Ser Val Thr Asn Ser  
260 265

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32

5 &lt;210&gt; 73

&lt;211&gt; 720

&lt;212&gt; DNA

10

&lt;213&gt; Nodularia spumigena NSOR10

15 &lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5)..(703)

20

&lt;223&gt;

25 &lt;400&gt; 73

gcgc atg cat cta gaa atg gcg atc gcc att att agt ata tgg gct atc  
 Met His Leu Glu Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile  
 1 5 10 15

49

30 agc cta ggt ttg tta ctt tat att gat ata tcc caa ttc aag ttt tgg  
 Ser Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp  
 20 25 30

97

35 atg ttg tta ccg ctc ata ttt tgg caa aca ttt tta tat acg gga tta  
 Met Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu  
 35 40 45

145

40 ttt att aca gct cat gat gcc atg cat ggg gta gtt ttt ccc aaa aat  
 Phe Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn  
 50 55 60

193

45 ccc aaa atc aac cat ttc att ggc tca ttg tgc ctg ttt ctt tat ggt  
 Pro Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly  
 65 70 75

241

50 ctt tta cct tat caa aaa ctt tta aaa aag cat tgg cta cat cac cat  
 Leu Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His  
 80 85 90 95

289

50 aat cca gcc agt gaa aca gat cca gat ttt cac aac ggg aag cag aaa  
 Asn Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys  
 100 105 110

337

aac ttt ttt gct tgg tat tta tat ttt atg aag cgt tac tgg agt tgg 385  
 Asn Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp  
 115 120 125

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tta caa att atc aca tta atg att att tat aac tta cta aaa tat ata 433  
 Leu Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile  
 130 135 140

10

tgg cat ttt cca gag gat aat atg act tat ttt tgg gta gtt ccc tca 481  
 Trp His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser  
 145 150 155

15

att tta agt tct tta caa tta ttt tat ttt gga act ttt cta ccc cac 529  
 Ile Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His  
 160 165 170 175

20

agt gag cct gta gaa ggt tat aaa gag cct cat cgt tcc caa act att 577  
 Ser Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile  
 180 185 190

25

agc cgt ccc att tgg tgg tca ttt ata act tgt tac cat ttt ggt tat 625  
 Ser Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr  
 195 200 205

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cat tac gaa cat cat gaa tac ccc cat gtt cct tgg tgg caa tta cca 673  
 His Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro  
 210 215 220

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gaa att tat aaa atg tct aaa tca aat ttg tgatctagag catgcgc 720  
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 225 230

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Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met  
 20 25 30



5 Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe  
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10 Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro  
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15 Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu  
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20 Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn  
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25 Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn  
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30 Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu  
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35 Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp  
     130                    135                    140

40 His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile  
     145                    150                    155                    160

45 Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser  
     165                    170                    175

50 Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser  
     180                    185                    190

Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His  
     195                    200                    205

Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu  
     210                    215                    220

Ile Tyr Lys Met Ser Lys Ser Asn Leu  
     225                    230